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RAW SEQUENCE LISTING

DATE: 09/11/2002

PATENT APPLICATION: US/10/051,618A

TIME: 10:31:46

Input Set : A:\seq listing.txt

Output Set: N:\CRF4\09112002\J051618A.raw

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3 <110> APPLICANT: Herath, Herath Mudiyansele
4 Athula Chandrasiri
5 Parekh, Rajesh Bhikhu
6 Patel, Thakorhhai Parshotambhai
7 Rohlf, Christian
9 <120> TITLE OF INVENTION: DPI-6, A PUTATIVE THERAPEUTIC TARGET AND BIOMARKER IN
NEUROPSYCHIATRIC AND
10 NEUROLOGICAL DISORDERS
12 <130> FILE REFERENCE: 2543-1-008/PCT US
14 <140> CURRENT APPLICATION NUMBER: US 10/051,618A
15 <141> CURRENT FILING DATE: 2001-10-24
17 <150> PRIOR APPLICATION NUMBER: GB 0004412.3
18 <151> PRIOR FILING DATE: 2000-02-24
20 <150> PRIOR APPLICATION NUMBER: GB 0004415.6
21 <151> PRIOR FILING DATE: 2000-02-24
23 <150> PRIOR APPLICATION NUMBER: GB 0006285.2
24 <151> PRIOR FILING DATE: 2000-03-15
26 <150> PRIOR APPLICATION NUMBER: GB 0028734.2
27 <151> PRIOR FILING DATE: 2000-11-24
29 <150> PRIOR APPLICATION NUMBER: US 09/724,391
30 <151> PRIOR FILING DATE: 2000-11-28
32 <150> PRIOR APPLICATION NUMBER: US 09/750,395
33 <151> PRIOR FILING DATE: 2000-11-28
35 <150> PRIOR APPLICATION NUMBER: GB 0030050.9
36 <151> PRIOR FILING DATE: 2000-12-08
38 <150> PRIOR APPLICATION NUMBER: US 60/254,830
39 <151> PRIOR FILING DATE: 2000-12-12
41 <160> NUMBER OF SEQ ID NOS: 5
43 <170> SOFTWARE: PatentIn version 3.0
45 <210> SEQ ID NO: 1
46 <211> LENGTH: 2479
47 <212> TYPE: DNA
48 <213> ORGANISM: Homo sapiens
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50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (1146)..(1146)
52 <223> OTHER INFORMATION: n=g or a or t or c at position 1146
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55 <221> NAME/KEY: CDS
56 <222> LOCATION: (38)..(1090)
58 <400> SEQUENCE: 1
59 ggcacgaggg ggcggcggct gcgggcgcag agcggag atg cag cgg ctt ggg gcc 55
60 Met Gln Arg Leu Gly Ala
61 1 5

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63	acc	ctg	ctg	tgc	ctg	ctg	ctg	gcg	gcg	gcg	gtc	ccc	acg	gcc	ccc	gcg	103
64	Thr	Leu	Leu	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Val	Pro	Thr	Ala	Pro	Ala	
65				10				15				20					
67	ccc	gct	ccg	acg	gcg	acc	tcg	gct	cca	gtc	aag	ccc	ggc	ccg	gct	ctc	151
68	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	Pro	Val	Lys	Pro	Gly	Pro	Ala	Leu	
69			25					30				35					
71	agc	tac	ccg	cag	gag	gag	gcc	acc	ctc	aat	gag	atg	ttc	cgc	gag	gtt	199
72	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn	Glu	Met	Phe	Arg	Glu	Val	
73		40					45				50						
75	gag	gaa	ctg	atg	gag	gac	acg	cag	cac	aaa	ttg	cgc	agc	gcg	gtg	gaa	247
76	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys	Leu	Arg	Ser	Ala	Val	Glu	
77	55				60					65				70			
79	gag	atg	gag	gca	gaa	gaa	gct	gct	gct	aaa	gca	tca	tca	gaa	gtg	aac	295
80	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Lys	Ala	Ser	Ser	Glu	Val	Asn	
81				75				80				85					
83	ctg	gca	aac	tta	cct	ccc	agc	tat	cac	aat	gag	acc	aac	aca	gac	acg	343
84	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Tyr	His	Asn	Glu	Thr	Asn	Thr	Asp	Thr	
85			90				95				100						
87	aag	gtt	gga	aat	aat	acc	atc	cat	gtg	cac	cga	gaa	att	cac	aag	ata	391
88	Lys	Val	Gly	Asn	Asn	Thr	Ile	His	Val	His	Arg	Glu	Ile	His	Lys	Ile	
89			105				110				115						
91	acc	aac	aac	cag	act	gga	caa	atg	gtc	ttt	tca	gag	aca	gtt	atc	aca	439
92	Thr	Asn	Asn	Gln	Thr	Gly	Gln	Met	Val	Phe	Ser	Glu	Thr	Val	Ile	Thr	
93		120				125				130							
95	tct	gtg	gga	gac	gaa	gaa	ggc	aga	agg	agc	cac	gag	tgc	atc	atc	gac	487
96	Ser	Val	Gly	Asp	Glu	Glu	Gly	Arg	Arg	Ser	His	Glu	Cys	Ile	Ile	Asp	
97	135			140			145			150							
99	gag	gac	tgt	ggg	ccc	agc	atg	tac	tgc	cag	ttt	gcc	agc	ttc	cag	tac	535
100	Glu	Asp	Cys	Gly	Pro	Ser	Met	Tyr	Cys	Gln	Phe	Ala	Ser	Phe	Gln	Tyr	
101			155				160			165							
103	acc	tgc	cag	cca	tgc	cgg	ggc	cag	agg	atg	ctc	tgc	acc	cgg	gac	agt	583
104	Thr	Cys	Gln	Pro	Cys	Arg	Gly	Gln	Arg	Met	Leu	Cys	Thr	Arg	Asp	Ser	
105			170				175			180							
107	gag	tgc	tgt	gga	gac	cag	ctg	tgt	gtc	tgg	ggt	cac	tgc	acc	aaa	atg	631
108	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Val	Trp	Gly	His	Cys	Thr	Lys	Met	
109			185				190			195							
111	gcc	acc	agg	ggc	agc	aat	ggg	acc	atc	tgt	gac	aac	cag	agg	gac	tgc	679
112	Ala	Thr	Arg	Gly	Ser	Asn	Gly	Thr	Ile	Cys	Asp	Asn	Gln	Arg	Asp	Cys	
113		200				205				210							
115	cag	ccg	ggg	ctg	tgc	tgt	gcc	ttc	cag	aga	ggc	ctg	ctg	ttc	cct	gtg	727
116	Gln	Pro	Gly	Leu	Cys	Cys	Ala	Phe	Gln	Arg	Gly	Leu	Leu	Phe	Pro	Val	
117	215			220			225			230							
119	tgc	aca	ccc	ctg	ccc	gtg	gag	ggc	gag	ctt	tgc	cat	gac	ccc	gcc	agc	775
120	Cys	Thr	Pro	Leu	Pro	Val	Glu	Gly	Glu	Leu	Cys	His	Asp	Pro	Ala	Ser	
121			235				240			245							
123	cgg	ctt	ctg	gac	ctc	atc	acc	tgg	gag	cta	gag	cct	gat	gga	gcc	ttg	823
124	Arg	Leu	Leu	Asp	Leu	Ile	Thr	Trp	Glu	Leu	Glu	Pro	Asp	Gly	Ala	Leu	
125			250				255			260							
127	gac	cga	tgc	cct	tgt	gcc	agt	ggc	ctc	ctc	tgc	cag	ccc	cac	agc	cac	871

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128 Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His
129          265          270          275
131 agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa      919
132 Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln
133      280          285          290
135 gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt      967
136 Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
137 295          300          305          310
139 ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg      1015
140 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
141          315          320          325
143 agc ctg act gaa gag atg gcg ctg ggg gag cct gcg gct gcc gcc gct      1063
144 Ser Leu Thr Glu Glu Met Ala Leu Gly Glu Pro Ala Ala Ala Ala Ala
145          330          335          340
147 gca ctg ctg gga ggg gaa gag att tag atctggacca ggctgtgggt      1110
148 Ala Leu Leu Gly Gly Glu Glu Ile
149          345          350
W--> 151 agatgtgcaa tagaaatagc taatttattt cccangtgt gtgctttaag cgtgggctga      1170
153 ccaggcttct tcctacatct tcttcccagt aagtttcccc tctggcttga cagcatgagg      1230
155 tgttgtgcat ttgttcagct cccccaggct gttctccagg cttcacagtc tgggtgcttg      1290
157 gagagtcagg cagggttaaa ctgcaggagc agtttgccac cctgtccag attattggct      1350
159 gctttgcctc taccagttgg cagacagccg tttgttctac atggctttga taattgtttg      1410
161 aggggaggag atggaaacaa tgtggagtc cctctgatt ggttttgggg aaatgtggag      1470
163 aagagtgcc tgctttgcaa acatcaacct ggcaaaaatg caacaaatga attttccacg      1530
165 cagttctttc catgggcata ggtaagctgt gccttcagct gttgcagatg aaatgttctg      1590
167 ttcaccctgc attacatgtg tttattcatc cagcagtggt gctcagctcc tacctctgtg      1650
169 ccagggcagc attttcatat ccaagatcaa ttccctctct cagcacagcc tggggagggg      1710
171 gtcattgttc tcctcgtcca tcagggattt cagaggctca gagactgcaa gctgcttgcc      1770
173 caagtcacac agctagttaa gaccagagca gtttcatctg gttgtgactc taagctcagt      1830
175 gctctctcca ctaccccaca ccagccttgg tgccaccaa agtgctcccc aaaaggaagg      1890
177 agaatgggat ttttcttttg aggcattgac atctggaatt aagggtcaaac taattctcac      1950
179 atccctctaa aagtaaaact ctgttaggaa cagcagtggt ctcacagtgt ggggcagccg      2010
181 tccttctaata gaagacaatg atattgacac tgcctctctt tggcagttgc attagtaact      2070
183 ttgaaaggta tatgactgag cgtagcatac aggttaacct gcagaaacag tacttaggta      2130
185 attgtagggc gaggattata aatgaaattt gcaaaatcac ttagcagcaa ctgaagacaa      2190
187 ttatcaacca cgtggagaaa atcaaaccga gcagggctgt gtgaaacatg gttgtaatat      2250
189 gcgactgcga aactgaact ctacgccact ccacaaatga tgttttcagg tgtcatggac      2310
191 tgttgccacc atgtattcat ccagagttct taaagtttaa agttgcacat gattgtataa      2370
193 gcatgctttc tttgagtttt aaattatgta taaacataag ttgcatttag aaatcaagca      2430
195 taaatcactt caactgctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2479
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 350
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo sapiens
203 <400> SEQUENCE: 2
205 Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
206 1          5          10          15
208 Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
209          20          25          30

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211 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
212          35                      40                      45
214 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
215          50                      55                      60
217 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
218 65                      70                      75                      80
220 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
221          85                      90                      95
223 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
224          100                     105                     110
226 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
227          115                     120                     125
229 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
230          130                     135                     140
232 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
233 145                     150                     155                     160
235 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
236          165                     170                     175
238 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
239          180                     185                     190
241 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
242          195                     200                     205
244 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
245          210                     215                     220
247 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
248 225                     230                     235                     240
250 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
251          245                     250                     255
253 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
254          260                     265                     270
256 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
257          275                     280                     285
259 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
260          290                     295                     300
262 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
263 305                     310                     315                     320
265 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
266          325                     330                     335
268 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
269          340                     345                     350
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 10
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 3
278 Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg
279 1                      5                      10
281 <210> SEQ ID NO: 4
282 <211> LENGTH: 10

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283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
W--> 285 <220> FEATURE:
286 <221> NAME/KEY: MOD_RES
287 <222> LOCATION: (3)..(3)
288 <223> OTHER INFORMATION: ASN residue is glycosylated
290 <400> SEQUENCE: 4
292 Val Gly Asn Asn Thr Ile His Val His Arg
293 1          5          10
296 <210> SEQ ID NO: 5
297 <211> LENGTH: 11
298 <212> TYPE: PRT
299 <213> ORGANISM: Homo sapiens
W--> 300 <220> FEATURE:
301 <221> NAME/KEY: MOD_RES
302 <222> LOCATION: (3)..(3)
303 <223> OTHER INFORMATION: ASN residue is glycosylated
305 <400> SEQUENCE: 5
307 Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg
308 1          5          10
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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1146

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

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L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1110
L:285 M:283 W: Missing Blank Line separator, <220> field identifier
L:300 M:283 W: Missing Blank Line separator, <220> field identifier